

What is claimed is:

1. A method of normalizing gene expression data wherein, in a process for comparing expression quantities with respect to a plurality of genes, which expression quantities have been obtained for a first sample, and expression quantities with respect to the plurality of the genes, which expression quantities have been obtained for a second sample, with each other, data concerning the expression quantities having been obtained for the second sample are normalized, the method comprising the steps of:

i) indicating the data concerning the expression quantities, which have been obtained for the first sample and the second sample, with points plotted on a logarithmic coordinate system, in which a horizontal axis represents logarithms of the expression quantities obtained for the first sample, and in which a vertical axis represents logarithms of the expression quantities obtained for the second sample,

ii) calculating a coefficient from a value of an intercept of an approximate straight line, which is obtained from approximate representation of the plotted points with a straight line having a slope of 1, on the vertical axis, and

iii) performing division processing for dividing the data concerning the expression quantities with respect to the plurality of the genes, which expression

quantities have been obtained for the second sample, by the coefficient, whereby the data concerning the expression quantities having been obtained for the second sample are normalized.

5 2. A method as defined in Claim 1 wherein the first sample is a sample obtained from a normal cell, and the second sample is a sample obtained from an abnormal cell.

10 3. A method of normalizing gene expression data wherein, in a process for comparing expression quantities with respect to a plurality of genes, which expression quantities have been obtained for a first sample, and expression quantities with respect to the plurality of the genes, which expression quantities have been obtained for
15 a second sample, with each other, data concerning the expression quantities having been obtained for the second sample are normalized, the method comprising the steps of:

20 i) indicating the data concerning the expression quantities, which have been obtained for the first sample and the second sample, with points plotted on a coordinate system, in which a horizontal axis represents the expression quantities obtained for the first sample, and in which a vertical axis represents the expression quantities obtained for the second sample,

25 ii) calculating a value of a slope of an approximate straight line, which is obtained from

approximate representation of the plotted points with a straight line passing through an origin of the coordinate system, and

5 iii) performing division processing for
dividing the data concerning the expression quantities with
respect to the plurality of the genes, which expression
quantities have been obtained for the second sample, by
the value of the slope of the approximate straight line,
whereby the data concerning the expression quantities
10 having been obtained for the second sample are normalized.

4. A method as defined in Claim 3 wherein the first sample is a sample obtained from a normal cell, and the second sample is a sample obtained from an abnormal cell.